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Copyright (c) 1993 - 2002
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Q8r2k3 mus musculu
Q9cyr0 mus musculu
016583 caenorhabdi
Q98qa6 mycoplasma
Q92dd9 llsteria in
Q88y8y2 listeria mo
Q4863y lactococcus
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Q4863y sulfolobus
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Q97kl3 clostridium
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Q9H8I7;
Q9H8I7;
Q1-MAR-2001 (TrembLrel. 16, Created)
Q1-MAR-2001 (TrembLrel. 16, Last sequence update)
Q1-MAR-2001 (TrembLrel. 16, Last annotation update)
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Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
Wagatsuma M., Hosolri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
"Ninomiya K., Iwayanagi T.;
"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AK02355; BAB14629.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA FLJ13593 fis, clone PLACE1009493.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishii K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml I.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Saakai H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Hayashiyaski Y., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Q1-JUN-2001 (TrEMBLrel.
Q1-JUN-2001 (TrEMBLrel.
4922443L0BRik protein.
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01-MAY-2000
01-MAY-2000
01-JUN-2002
                                                                                                         Pyrococcus abyssi.
Archaea; Euryarchaeota;
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EMBL; AKO16573; BAB30314.1; -.
MGD; MGI:1921674; 4932443L08Rik.
SEQUENCE 757 AA; 87667 MW; 320D61A71
                                                                                  Pyrococcus
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Mammalia; Eutheria; Rodentia;
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(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
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                                                                                                            Thermococci;
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Last
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                                                                                                                                                                                                                                                                                                                                  Created)
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                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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4.7e-33;
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Query Match
Best Local Similarity
"~+~hes 8; Conserv
Q97KL3;
01-OCT-2001
01-OCT-2001
01-MAR-2002
ATPase with
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ248288; CAB50678.1; -.

InterPro; IPR005242; Cons_hypoth374.

Pfam; PF03706; UPF0104; 1.

TIGRFAMs; TIGR00374; TIGR00374; 1.

Hypothetical protein; Complete proteome.

SEQUENCE 335 AA; 37288 MW; F29086681DAFCFFF CRC64;
                                                                                                                                                                                                                                                    Pfam; PF01827; DUF38; 1.
Pfam; PF00646; F-box; 1.
SMART; SM00256; FBOX; 1.
PROSITE; PS50181; FBOX; 1.
SEQUENCE 351 AA; 40374 MW;
                                                                                                                                                                                                                                                                                                                                                  investigating biology.";
Science 282:2012-2018(1998).
EMBL; Z81554; CAB04503.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhabditidae; Peloderinae; NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans
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01-DEC-2001
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Heilig R.;
                                                                                                                                                                                                                                                                                                                         InterPro; IPR002900; DUF38.
InterPro; IPR001810; F-box.
                                                                                                                                                                                                                                                                                                                                                                                              "Genome sequence of the nematode
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                                                                                                                                                                     172 DGSLDLRS 179
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  chaperon
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                                                                       PRELIMINARY;
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Last sequence update)
Last annotation update)
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Pred. No.
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Pred. No
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  domains,
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Best Local
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Q95KK4;
                                                                                                                                                                                                                                 Signal.
SIGNAL
                                                                                                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                                                       InterPro; IPR000424; SSB_protein. Pfam; PF00436; SSB; 1. TIGRFAMS; TIGR00621; ssb; 1.
                                                                                                                                                                                                                                                                                                                                                                                              "Identification and expression of cDNA and pseudogene coding "Identification and expression of cDNA and pseudogene coding rabbit mitochondrial single-strand DNA-binding protein."; Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ311162; CAC38115.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-JUN-2002 (TrEMBLrel. 21,
Single-stranded DNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q., Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I., Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M., Bennett G.N., Koonin E.V., Smith D.R.; Bennett G.N., Koonin E.V., Smith D.R.; "Genome sequence and comparative analysis of the solvent-producing "Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum."; J. Bacteriol. 103:4823-4838(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00300; CLPPROTEASEA. SMART; SM00382; AAA; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003959; AAA_ATPase_centr.
InterPro; IPR001370; Chaprnin_clpA/B.
Pfam; PF00004; AAA; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN-ATCC 824 /
                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATP-binding; Complete proteome. SEQUENCE 752 AA; 84925 MW;
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MEDLINE-21359325; PubMed-11466286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clostridium acetobutylicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 IINEGKDK 131
                                            151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               678 IINEGKDK 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6
  22
                                            SSLVLER 157
  SSLVLER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
8; Conserv
                                                                                                              Similarity
                                                                                                                                                                                                                                                                                PS00735;
PS00736;
                                                                                                                                                                              1
17
148
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                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
28
                                                                                                                                                                                     ΑĄ;
                                                                                                                                                                                                                                                                           SSB_1; UNKNOWN_1.
SSB_2; UNKNOWN_1.
                                                                                                                                                                                   16
148
17155
                                                                                                           3.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.2%;
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Last annotation update)
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                                                                                        0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   precursor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 8;
                                                                                     Score 7; DB 6
Pred. No. 32;
0; Mismatches
                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57B4C4B6C47D80A6 CRC64;
                                                                                                                                                                                   9AF894B6468C6C43 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ₹
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                                                                                                                DB 6
o. 32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B
                                                                                                                                      6;
                                                                                                                                    Length 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                        0,:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 752;
                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P., Daly M.J.,
                                                                                     0;
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                                                                                     Gaps
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RESULT 7
Q8R2K3
ID Q8R2
AC Q8R2
DT 01-4
DT 01-4
DT 01-4
OC Euk
OC Euk
OC Mam
OX NCE
RP SE(
RC TI)
RP SE(
RC TI)
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Q9CYR0
밁
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                                                                                                                                                     RC STRAIN-C79EL/60; TISSUE-EMBRYO;
RX MEDLINE-21085660; pubMed-11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Kawai J., Shinagawa A., Shibata Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Ra Brownstein M.J., Bult C., Fletcher C., Fujita M., Washio T.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Horostein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Holling J., Wombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Holling R., Kohtsuki S.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
               "Functional annotation of a f
Nature 409:685-690(2001).
EMBL; AK013425; BAB28850.1; -
HSSP; Q04837; 3ULL.
MGD; MGI:1920040; 2810480P10R
InterPro; IPR000424; SSB_prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QBR2K3;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to single-stranded DNA binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9CYRO;
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2810480P10Rik protein.
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EMBL; BC0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8R2K3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                            Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2810480P10RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=MAMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 SSLVLER 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tted (APR-2002) to the EMBL/GenBank/DDBJ databases
BC028648; AAH28648.1; -.
NCE 148 AA; 17157 MW; E5C00016DF6BB4CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (APR-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Mouse).
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                                     2810480P10Rik
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
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Pred. No.
                                                                                                                        full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Ver
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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). 32;
                                                                                                                           mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vertebrata; Euteleostomi;
thi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          update)
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                                                                                                                        collection.";
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RESULTANCE OF CASE OF SAME OF 
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Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ol-DEC-2001 (TrEMBLrel. 05, Create 01-DEC-2001 (TrEMBLrel. 19, Last an Hypothetical 19.8 kDa protein C33C12.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
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STRAIN-BRISTOL N2;
STRAIN-BRISTOL N2;
Cattung S., Scheet P.;
Cattung S.,
                                                                                                                                                                         Q98QA6
Q98QA6;
01-0CT-2001
01-0CT-2001
01-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGRFAMS;
PROSITE; P
PROSITE; P
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Direct Submission.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ EMBL; AF016662; AAB66062.1; -.
Hypothetical protein.
SEQUENCE 170 AA; 19762 MW; D6C3E6F4BEDE52I
                                                     Mycoplasma pulmonis.
Bacteria; Firmicutes; Bacillus/Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  None;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Rhabditidae; Pelode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             016583
                                                                                                                    MYPU_4600.
                                                                                                                                             Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Waterston R.;
Mycoplasmataceae;
NCBI_TaxID=2107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151 SSLVLER 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          FLIEKLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  s; TIGR00621; ssb; 1
; PS00735; SSB_1; 1.
; PS00736; SSB_2; 1.
E 152 AA; 17319 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 7; Conserv
                                                                                                                                          (TrEMBLrel. 18, Created)
(TrEMBLrel. 18, Last sequence update)
(TrEMBLrel. 18, Last annotation update)
1 protein MYPU_4600.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget (
Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson I
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell I
Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
"Comparative genomics of Listeria species.";
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SEQUENCE FR
STRAIN=UAB
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Blanchard A.;
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STRAIN=CLIP 11262 / SEROVAR
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NCBI_TaxID=1642;
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Chambaud I., Heilig R., Ferris S., B
Moszer I., Dybvig K., Wroblewski H.,
                                                                                                                                                             Hypothetical protein; Compact SEQUENCE 202 AA; 22393
                                                                                                                                                                                 InterPro; IPR000379; Ser_estrs_site.
                                                                                                                                                                                                          Science 294:849-852(2001).
EMBL; AL596166; CAC95986.1; -.
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Nucleic Acids Res. 2
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CAC13633.1; -.
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Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
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Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
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Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
"Comparative genomics of Listeria species.";
Science 204.440-873/2001
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Listeriaceae; Listeria.
                                                                                                                                                                                                         Appl. Environ. Microbiol. 61:1082-1089(1995). EMBL; U17255; AAC43329.1; -.
                                                                                                                                                                                                                                                    Siegers K., Entian K.D.; "Genes involved in immunity to the lantibiotic lactis 6F3.";
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EMBL; AL591976; CAC98838.1; -.
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MEDLINE=21537279; PubMed=11679669;
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Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
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InterPro; IPR000379; Ser_estrs_site.
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RESULT 14
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Q48637;
01-NOV-1996 (TrEMBLrel. C
01-NOV-1996 (TrEMBLrel. C
01-DEC-2001 (TrEMBLrel. )
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Q96XL5;
01-DEC-2001
01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                    Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S., Sekine M., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A., Oshima T., Kikuchi H.;
                                                                                                                                                               Hypothetical protein; Complete SEQUENCE 231 AA; 26846 MW;
                                                                                                                                                                                                                        "Complete genome sequence of an aerobic thermoacidophilic Crenarchaeon, Sulfolobus tokodaii strain7.";
DNA Res. 8:123-140(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sulfolobus tokođaii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lactococcus lactis.
Bacteria; Firmicutes; Bacillus
Streptococcaceae; Lactococcus.
NCBI_TaxID=1358;
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                                                                                                                                                                                                           EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                      IINEGKD 130
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                                                                               Similarity 7; Conserv
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229
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100.0%; Pr
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24174 MW;
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Pred. No. 44;
0; Mismatches
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Last sequence update)
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Pred. No
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F59852E1099E7CD1 CRC64;
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RESULT 16

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SMART; SM00382; AAA; 1.
PROSITE; PS00211; ABC_TRANSPORTER; 1.
ATP-binding; Transport.
ATP-binding; Transport.
SPROUENCE 244 AA; 26709 MW; 785452
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050296;
01-JUN-1998
01-JUN-1998
01-JUN-2002
ATP-binding
                                                                                   SEQUENCE FROM N.A. 7120;
STRAIN-PASTEUR C NO. 7120;
MEDLINE-95095923; PubMed-8002578;
Maldener I., Fiedler G., Ernst A., Fernandez-Pinas F., Wolk C.P.
"Characterization of devA, a gene required for the maturation of proheterocysts in the cyanobacterium Anabaena sp. strain PCC 712
J. Bacteriol. 176:7543-7549(1994).
SEQUENCE FROM N.A.

MEDLINE-21595285; PubMed-11759840;

Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,

Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura '

Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,

Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
                                                                                                                                                                                                                                                                                               O57281 PRELIMINARY: PRT; 244 AA.
O57281;
O1-NOV-1996 (TrEMBLrel. O1, Created)
O1-NOV-1996 (TrEMBLrel. O1, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
PCC7120 DEVB, DEVA genes, ORF2 & ORF3 (Heterocyst specific ABC-transporter, ATP-binding subunit).
DEVA OR ALR3712.
                                                                                                                                                                                             Fiedler G., Arnold M
Submitted (AUG-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003439; ABC_transportr.
Pfam; PF00005; ABC_tran; 1.
ProDom; PD000006; ABC_transportr; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a putative ABC transporter in the cyanoba ATCC 29413. ", BIOChim. Blophys. Acta 1375:140-143(1998) -1- SIMILARITY: BELONGS TO THE ABC TRANSP EMBL; AJ003195; CAA05977.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-ATCC 29413;
STRAIN-ATCC 29413;
MEDLINE-98440130; PubMed-9767151;
Fiedler G., Arnold M., Maldener I.;
"Sequence and mutational analysis o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anabaena variabilis.
Bacteria; Cyanobacteria;
NCBI_TaxID=1172;
                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                      STRAIN-PCC7120;
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the EMBL/GenBank/DDBJ
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Nostocales;
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baena variabilis
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Best Local
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Nucleic Acids Res. 29:2145-2153(
EMBL; AL445563; CAC13294.1;
MypuList; MYPU_1210; -
Hypothetical protein; Complete p
SEQUENCE 245 AA; 28756 MW; 5
                             047800;
01-JUN-1998
01-JUN-1998
01-DEC-2001
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01-0CT-2001
01-0CT-2001
Gymnodraco acuticeps
           CYTB.
                     Cytochrome
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Moszer I., Dybvig K., Wroblewski H.,
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-UAB CTIP;
                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein MYPU_1210.
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SMART; S
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InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003439; ABC_transportr.
Pfam; PF00005; ABC_tran; 1.
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DNA Res. 8:205-213(2001)
-!- SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                             Blanchard A.;
                                                                                                                                                                                                                                                                                                       MEDLINE=21267165; PubMed=11353084;
                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                              Mycoplasma pulmonis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATP-binding; Transport; Comple SEQUENCE 244 AA; 26723 MW;
                                                                                                                                                                                                                                                               "The complete genome sequence of the murine
                                                                                                                                                                                                                                                                                                                                                          Mycoplasmataceae;
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PROSITE; PS00211; ABC_TRANSPORTER; 1.
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                 (TrEMBLrel. () (TrEMBLrel. () (TrEMBLrel. () b (Fragment).
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(TTEMBLrel. 18, Last sequence up
(TTEMBLrel. 18, Last annotation
protein MYPU_1210.
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(Antarctic dragonfish).
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23 MW; 34182185A65C0A4B CRC64;
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Pred. No.
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                              update)
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065045;
01-AUG-1998 (TIEMBLITEL 0
01-AUG-1998 (TIEMBLITEL 0
01-JUN-2002 (TIEMBLITEL 2
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                                                                                                                                                       characterization and analysis of linkage in b genetics 149:1089-1098(1998).
Genetics TAB:1008-1098(1998).
-I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE P-I- SIMILARITY: BELONGS TO THE MIP/AQUAPORIN EMBL; AF051202; AAC32107.1; -.
HSSP; P29972; 1FOY.
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-98278823; PubMed-9611216;
Perry D.J., Bousquet J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Picea mariana (Black spruce).
Eukaryota; Viridiplantae; Streptophyta; Eml
Spermatophyta; Coniferopsida; Coniferales;
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(In) di Prisco G., Pisano E., Clarke A. (eds. FISHES OF ANTARCTICA. A BIOLOGICAL OVERVIEW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen W.J., Bonillo C., Lecointre G.; "Phylogeny of the Channichthyidae (Notothenioidei,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neot Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Notothenioidei; Bathydraconidae; Gymnodraco.
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                                                                                              Pfam; PF00230; MIP;
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0; Mismatches
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                                                                                                                                                                                                                           MEMBRANE PROTEIN
/AQUAPORIN FAMILY
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Euteleostei; Neoteleostei;
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es; Pinaceae;
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Picea.
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01-JAN-1998
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UDP-glucose
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E., Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D., Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C., Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S., Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L., Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T., Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
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01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                               STRAIN=VC-16 / DSM 4304 / ATCC 49558; MEDLINE=98049343; PubMed=9389475;
                                                                                                                                                                                                                                                                             Archaeoglobus fulgidus.
Archaea; Euryarchaeota;
Archaeoglobaceae; Archa
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Porin; Transmembrane; Transport.
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                                                                                                                                                                                                                                                            NCBI_TaxID=2234;
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Matches 7
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Best Local S
Matches 7
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O93259;
O1-NOV-1998 (TrEMBLrel. 08, C
O1-NOV-1998 (TrEMBLrel. 08, L
O1-MAR-2002 (TrEMBLrel. 20, L
Melanocortin 3-receptor.
                                                            Q9XXA9;
Q1-NOV-1999 (TrEMBLrel 12, C
Q1-NOV-1999 (TrEMBLrel 12, I
Q1-MAR-2002 (TrEMBLrel 20, I
Y94A7B.5 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Takeuchi S., Takahashi S.;

"A possible involvement of melanocortin 3-receptor in the of adrenal gland function in the chicken.";

Biochim. Biophys. Acta 1448:512-518(1999).

-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TICR: ARUNYA, TI
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InterPro: IPRO00276; GPCR_Rhodpsn.

Pfam; PF00001; 7tm_1; 1.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.

G-PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Melanocutta. Gallus (Chicken).

Gallus gallus (Chicken).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-WHITE LEGHORN;
MEDIANE-99144114; PubMed-9990303;
Takeuchi S., Takahashi S.;
                                                                                                                                                                                                                                                      Q9XXA9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                reducing archaeon Archaeoglobus fulgidus.
Nature 390:364-370(1997).
EMBL; AE001084; AAB90929.1; -.
                            Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9031;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                      PRELIMINARY;
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100.0%; Pr
      Nematoda;
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Pred. No.
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Chromadorea;
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on update)
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Rhabditida;
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Best Local S
Matches 7
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C STRAIN-ATCC 35210 / B31;

C STRAIN-ATCC 35210 / B31;

X MEDLINEE-98065943; PubMed-9403685;

X MEDLINEE-98065943; PubMed-9403685;

A Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.

A Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K.,

A Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,

A Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Han

A Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Han

A Van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,

A Utterback T., Waithey L., McDonald L., Artiach P., Bowman C.,

A Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatc
                                                                                   Query Match
Best Local Similarity
Matches 7; Conserv
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01-JUN-1998
01-MAR-2002
                                                                                                                                                                                                                                                                                                                           burgdorfer1.";
Nature 390:580-586(1997).
NATURE 390:163; AAC66977.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        investigating biology."; Science 282:2012-2018(1998). Science 282:2012-2018(1998). EMBL; AL023856; CAA19567.1; -. InterPro; IPRO03003; 7TM_chemo2. InterPro; IPRO00168; 7TM_nematode. Pfam; PF01604; 7tm_5; 1. SEQUENCE 327 AA; 37108 MW; B251B168CC77BBBD CRC64;
                                                                                                                                                                               Pfam; PF02272; DHHA1; 1.
Hypothetical protein; Complete
SEQUENCE 330 AA; 37377 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  051564;
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InterPro; IPR001667;
Pfam; PF01368; DHH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Spirochaetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Borrelia burgdorferi (Lyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BB0619
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NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                      TIGR; BB0619;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=139;
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139
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                          FLIEKLI 139
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3 (TrEMBLIEL. 06, 1
2 (TrEMBLIEL. 20, 1
al protein BB0619.
                                                                                       Conservative
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                                                                                                             3.7%;
100.0%;
                                                                                                                                                                                                                                                                                                 DHHA1
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Spirochaetaceae; Borrelia
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392DB8DF6160DEA6 CRC64;
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01-MAR-2002 (TrEMBLrel. 20, C
01-MAR-2002 (TrEMBLrel. 20, I
01-MAR-2002 (TrEMBLrel. 20, I
Periplasmic binding protein c
PHND OR Z5707 or ECS5087.
Escherichia coli 0157:H7.
                               STRAIN-0157:H7 / RIMD 0509952;

MEDLINE-21156231; PubMed-11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoya Hayashi T., Makino E., Nakayama K., Murata T., Tanaka M., Tobe J Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunag Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001).
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"The smcL gene of Listeria ivanovii encodes mediates bacterial escape from the phagocytimol. Microbiol. 33:510-523(1999).
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01-MAY-2000
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Listeriaceae; Listeria.
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Listeria ivanovii.
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                                                                                                                                                                                                                                                                               "Genome sequence of enterohaemorrhagic Nature 409:529-533(2001).
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MEDLINE-21074935; PubMed-11206551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN-0157:H7 / E
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Welch R.A., Blattner F.R.;
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Pro; IPR005135; Exo_endo_phos.
                      AE005643;
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AA; 38455 MW;
                    AAG59304.1;
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46F398E58A8434D7 CRC64;
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Tobe T.,
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01-OCT-2001
01-OCT-2001
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                                             STRAIN-MAFF303099;
MEDLINE-21082930; PubMed-11214968;
MEDLINE-21082930; PubMed-11214968;
Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto
Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
Watanabe A., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
Kishida Y., Kiyokawa C., Kohara M., Shimpo S., Sugimoto M.,
Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
Takeuchi C., Yamada M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=ATCC 29253;
MEDLINE-98085969; PubMed-9426000;
Ruan X., Stassi D., Lax S.A., Katz L.;
"A second type-I PKS gene cluster isolated from hygroscopicus ATCC 29253, a rapamycin-producing Gene 203:1-9(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomyces hygroscopicus.
Streptomyces hygroscopicus.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            "Complete genome structure Mesorhizobium loti."; DNA Res. 7:331-338(2000).
                                                                                                                                                                  Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; alpha subd
Phyllobacteriaceae; Mesorhizobium.
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Pfam; PF01042; UPF0076; 1.
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NCBI_TaxID=1912;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence up
01-MAR-2002 (TrEMBLrel. 20, Last annotation
Putative pteridine-dependent dioxygenase.
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0; Mismatches
                                    the nitrogen-fixing
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                                                                                                                                                                                                                                                                              344
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66;
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                                                                                                                                                                               Rhizobiaceae
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                                    symbiotic
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                                                                                                                                                                               group;
                                     bacterium
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Best Local S
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InterPro; IPR001064; Crystallin.
Pfam; PF02653; BPD_transp_2; 1.
PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
SEQUENCE 344 AA: 36001 ...
                                                                                                                                 Q9MKL8;
01-OCT-2000
01-OCT-2000
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U1-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical cytosolic protein FN0719.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8RFH8;
                                                                                                                                                                                                                                                                                                                          Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lyk Bhattacharyya A., Bartman A., Gardner W., Garchkin G., Zhu I. Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R., Fonstein M., Kyrpides N., Overbeek R.; "Genome sequence and analysis of the oral bacterium Fusobact nucleatum strain ATCC 25586.", J. Bacteriol 184:2005-2018(2002).
                                                                                                               ND5
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-ATCC 25586;
PubMed-11889109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fusobacterium nucleatum Bacteria; Fusobacteria;
          STRAIN-F;
Prueser F.,
                               SEQUENCE FROM N.A.
                                                                      Pterygota;
                                                                               Eukaryota;
                                                                                         Mitochondrion.
                                                                                                   Carabus abbreviatus
                                                                                                                       NADH dehydrogenase
                                                                                                                                                                         Q9MKL8
                                                                                                                                                                                                                                                                                                                    Complete
                                                  NCBI_TaxID=114446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=76856;
 "Colonization
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                                                                                                                                                                                                                                                                                                        proteome;
350 AA;
                                                                     Neoptera;
                                                                               Metazoa;
                                                                                                                      (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 20, Last annotation updat
ogenase subunit 5 (Fragment).
           Brueckner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.7%; S llarity 100.0%; Conservative 0;
                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                         PRELIMINARY;
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Canary Is
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41804 MW; 21A901CF46CD50D8
                                                                              Arthropoda;
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                                                                      Endopterygota;
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         Mossakowski
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                                                                    Tracheata; Hexap
ota; Coleoptera;
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 Carabus
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          D.;
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5. 67;
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 species: evidence
                                                                             Hexapoda;
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                                                                     Adephaga;
                                                                                                                                                                                                                                                                                                         CRC64;
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Zhu
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Matches 7
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Best Local
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-i-CATALYTIC ACTIVITY: NADH + UBIC EMBL; AB039808; BAA92457.1; -
EMBL; AB039804; BAA92453.1; -
EMBL; AB039805; BAA92454.1; -
EMBL; AB039805; BAA92455.1; -
EMBL; AB039805; BAA92455.1; -
EMBL; AB039805; BAA92456.1; -
EMBL; AB039805; BAA92456.1; -
EMBL; AB039806; BAA92466; BAA92466; BAA92466; BAA92466; BAA92466; BAA92466; BAA92466; BAA92466; B
                     Q9MEG6;
01-OCT-2000
01-OCT-2000
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    different character complexes.";
(In) Brandmayr P., Lovei G., Brandmayr T.Z., Caviga Taglianti A. (eds.);
Natural history and applied ecology of carabid the 9th European carabidologist meeting), pp.1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9MEG7;
01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -|- CATALYTIC ACTIVITY: NADH + UB
EMBL; AF231695; AAF61942.1; -
InterPro; IPR001750; Oxidored_q1.
Pfam; PF00361; oxidored_q1; 1.
 NADH dehydrogenase
                                                                                                  Q9MEG6
                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                    Mitochondrion; NAD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-VARIOUS STRAINS; TISSUE-THORAX MUSCLE; Su Z.H., Tominaga O., Saito S., Kim C.G., Osawa "Phylogeny of Tomocarabus opaculus (Coleoptera,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                     NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from mitochondrial ND5 gene sequences
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Similarity 100.0%
7; Conservative
                   (TrEMBLrel.) (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                               355 AA;
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                                                                                                                                                                                                                                                                        Conservative
                                                                                                PRELIMINARY;
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Lrel. 15, Created)
Lrel. 15, Last sequence update)
Lrel. 20, Last annotation update
subunit 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lrel. 15, Created)
Lrel. 15, Last sequence up
Lrel. 20, Last annotation
subunit 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                             40947
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rthropoda; Tracheata; Hexapoda; Insecta;
Endopterygota; Coleoptera; Adephaga; Carabidae;
                                                                                                                                                                                                                                                                                        100
                                                                                                                                                                                                                                                                                                             3.7%;
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Pred. No
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Pred. No
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Carabidae)
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Pfam; PF00361; oxidored_q1; 1.
Mitochondrion; NAD; Oxidoreductas
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EMBL; AB039807; BAA92456.1; -
                                                                            SEQUENCE
                                                                                                              InterPro; IPR001750; Oxidored_q1.
Pfam; PF00361; oxidored_q1; 1.
Mitochendrion; NAD; Oxidoreductas
                                                                                                                                                                                  EMBL; AB041069; BAA94628.1; -
EMBL; AF219473; AAF62460.1; -
                                                                                                                                                                                                                        Syst. Biol. 0:0-0(2000).
-!- CATALYTIC ACTIVITY: NADH + UBIQUINONE
                                                                                                                                                                                                                                               beetles Ohomopterus.";
Syst. Biol. 0:0-0(2000).
                                                                                                                                                                                                                                                                                                                                                                                                 Toninaga O., Su Z.H., Kim C.G., Okamoto M., Imura Y., Osawa S.; "Formation of the Japanese Carabina Fauna inferred from a phylogenetic tree of mitochondrial ND5 gene sequences (Coleoptera, Carabidae)."; J. Mol. Evol. 50:541-549(2000).
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Pterygota; Neoptera;
                                                                                                                                                                                                                                                                                                                     Sota T., Vogler A.P.;
                                                                                                                                                                                                                                                                                                                                         STRAIN-OH33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-55; TISSUE-THORAX MUSCLE;
MEDLINE-20296815; PubMed-10835484;
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                                                                          40873 MW;
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01-OCT-2000
01-OCT-2000
01-MAR-2002
SEQUENCE FROM N.A.
STRAIN-37, 33, 34, AND 36; TISSUB-THORAX MUSCLE;
Kim C.G., Tominaga O., Su Z.H., Osawa S.;
"Origin and Diversification of Euleptocarabus porrecticollis (Coleoptera, Carabidae) in the Japanese Islands inferred from Mitochondrial ND5 Gene Sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AB041059; BAA94618.1; --
EMBL; AB041054; BAA94613.1; --
EMBL; AB041056; BAA94615.1; --
EMBL; AB041057; BAA94615.1; --
EMBL; AB041057; BAA94617.1; --
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STRAIN=35, 31, 33, 36, AND 34; TISSUE=THOF
STRAIN=32026815; PubMed=10835484;
Tominaga O., Su Z.H., Kim C.G., Okamoto M.
Tominaga O., Su Z.H., Kim C.G., Okamoto M.
Tomination of the Japanese Carabina Fauna
tree of mitochondrial ND5 gene sequences
J. Mol. Evol. 50:541-549(2000).
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Pterygota;
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01-OCT-2000 (TrEMBLITEL 15, Last sequenc
01-MAR-2002 (TrEMBLITEL 20, Last annotat
NADH dehydrogenase subunit 5 (Fragment).
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Best Local
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EMBL; AB022586; BAA74499.1; --
EMBL; AB022587; BAA74499.1; --
EMBL; AB022587; BAA74499.1; --
Interpro; IPR001750; Oxidored_q1.
pfam; pF00361; oxidored_q1; 1.
Milochondrion; NAD; Oxidoreductase; Ub
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000
01-OCT-2000
01-MAR-2002
                                                                                                         01-OCT-2000
01-MAR-2002
                                                                                                                                               Q9MDT2;
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AB039800; BAA92449.1; --
EMBL; AB039796; BAA92445.1;
InterPro; IPR001750; Oxidored
Pfam; PF00361; Oxidored_q1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mitochondrion
                                                                                   NADH dehydrogenase
                                                                                                                                                                                          Q9MDT2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carabus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota;
Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9MDZ5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9MDZ5
                                          Carabus porrecticollis kansaiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=118064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carabus opaculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NADH dehydrogenase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mitochondrion; NAD;
                                                                                                                                                                                                                                                                                               157
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                                                                                                                                                                                                                                                                                                                                      20 FIFLLFF 26
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                                                                                                                                                                                                                                                                                             |||||||
FIFLLFF 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FIFLLFF 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7; Conserv
                                                                                                                                                                                                                                                                                                                                                                               Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Metazoa; /
Neoptera;
  Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            355 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 355 AA;
                                                                           (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 20, Last annotation updat
ogenase subunit 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
ogenase subunit 5 (Fragment).
                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACTIVITY: NADH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Evol. 0:0-0(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arthropoda; Tracheata; Hexapoda; Insecta; Endopterygota; Coleoptera; Adephaga; Carabidae;
  Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oxidoreductase; Ubiquinone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              40899 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40914 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oxidored_q1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.7%;
                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 7; DB 8; Pred. No. 68; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                               0,
                                                                                                                                                                                                                                                                                                                                                                                                Score 7;
Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 + UBIQUINONE = NAD(+) + UBIQUINOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67A294D3AE3C4B30 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              704B4C5FBCAl3D00 CRC64;
                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                            No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           355
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                                                                                                                                                                                        AA
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                                                                                                       update)
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                                                                                                                                                                                                                                                                                                                                                                                                                     Length 355;
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                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Query Match
Best Local Similarity
Thes 7; Conserve
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Q9MDT0
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-23, AND 22; ILSSUE-INVA..... Sawa S.;
Kim C.G., Tominaga O., Su Z.H., Osawa S.;
"Origin and Diversification of Euleptocarabus
"Origin and Diversification of Euleptocarabus
                                                                                                                                                                                                                                                                                                                          tree of mitochondrial ND5 gene sequences (Coleoptera, J. Mol. Evol. 50:541-549(2000).

-I- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UEMBL, AB041073; BAA94632.1; -.
EMBL, AB041070; BAA94632.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=45, 43, AND 39; TISSUE=THOR
MEDLINE=20296815; PubMed=10835484;
Tominaga O., Su Z.H., Kim C.G., Ok
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001750; Oxidored_q1.
Pfam; PF00361; oxidored_q1; 1.
Mitochondrion; NAD; Oxidoreductase;
NON_TER
                                                                                                                                                                                                                InterPro; IPR001750; Oxidored_q1.
pfam; pF00351; oxidored_q1; 1.
Mitochondrion; NAD; Oxidoreductase;
NON_TER
1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-MAR-2002 (TrEMBLrel. 20, NADH dehydrogenase subunit 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Coleoptera, Carabidae) in the Japanese Islands Mitochondrial ND5 Gene Sequences."; Mol. Phylogenet. Evol. 0:0-0(1999).
-!- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(
                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                           EMBL; AB041071;
                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-20296815; Pubmeu=1003000; Okamoto M., Imura Y., Osawa S.; Tominaga O., Su Z.H., Kim C.G., Okamoto M., Imura Y., Osawa S.; Formation of the Japanese Carabina Fauna inferred from a phylogenetic profits of the Japanese Carabina Fauna (Coleoptera, Carabidae).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carabus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carabus granulatus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=118799;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AB022576; BAA74488.1; -. EMBL; AB022575; BAA74487.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN=23, AND 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pterygota; Neoptera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=87296;
157 FIFLLEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 157 FIFLLFF 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39
                                            20 FIFLLFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 FIFLLFF 26
                                                                                                                                                                                        355 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neoptera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         355 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Metazoa;
                                                                                             Conservative
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163
                                              26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AND 39; TISSUE=THORAX MUSCLE;
                                                                                                                                                                                                                                                                                                        BAA94630.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-THORAX MUSCLE;
O., Su Z.H., Osawa S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arthropoda; Tracheata; Hexapoda; Insecta; Endopterygota; Coleoptera; Adephaga; Car
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40944 MW;
                                                                                                                                                                                        40803 MW;
                                                                                                                100.0%;
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                                                                                                                                           3.7%;
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Last sequence update)
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Pred. No.
                                                                                                                                      Score 7;
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                                                                                                                   Pred. No.
                                                                                                                                                                                          8BC0FEE5FFB605A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                UBIQUINONE - NAD(+) + UBIQUINOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8A2E3165B68D5F10 CRC64;
                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                      Ubiquinone
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68;
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                                                                                                                                           Length 355;
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                                                                                             Indels
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                                                                                          Gaps
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RESULT Q9MDS6

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RESULT OPENING OF THE PROPERTY OF THE PROPERTY
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Best Local S
Matches 7
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                    SEQUENCE FROM N.A.
STRAIN-49, AND 47; TISSUE-THORAX MUSCLE;
MEDLINE-20296815; PubMed-10835484;
Tominaga O., Su Z.H., Kim C.G., Okamoto M., Imura Y., Os
"Formation of the Japanese Carabina Fauna inferred from
tree of mitochondrial ND5 gene sequences (Coleoptera, Ca
J. Mol. Evol. 50:541-549(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9MDR6;
01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                        Carabus
                                                                                                                                                                                                                                                                                                                                                                    Mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                  Carabus granulatus
                                                                                                                                                                                                                                                                                                                                                                                                                                  Ŋ5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mol. Phylogenet. Evol. 0:0-0(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mitochondrial ND5 Gene Sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carabus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pterygota; Neoptera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000 (TrEMBLrel. 01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                               Pterygota; Neoptera;
                                                                                                                                                                                                                                                                                                                                             Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kim C.G., Tominaga O., Su Z.H., Osawa S., "Origin and Diversification of Euleptocarabus (Coleoptera, Carabidae) in the Japanese Island
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=VARIOUS STRAINS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carabus porrecticollis kansaiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NADH dehydrogenase subunit 5
                                                                                                                                                                                                                                                       NCBI_TaxID=118799;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=87296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 FIFLLFF 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L; AB022585; BAA74497.1;
AB022571; BAA74483.1;
L; AB022573; BAA74485.1;
L; AB022574; BAA74486.1;
L; AB022578; BAA74490.1;
AB022579; BAA74491.1;
L; AB022580; BAA74491.1;
AB022580; BAA74493.1;
AB022581; BAA74493.1;
AB022581; BAA74493.1;
L; AB022581; BAA74494.1;
L; AB022581; BAA74495.1;
L; AB022581; BAA74494.1;
L; AB022581; BAA74495.1;
L; AB02581; BAA74495.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||||||
| FIFLLEF 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PF00361; oxidored_q1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR001750; Oxidored_q1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Metazoa; Arthropoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               355 AA;
                                                                                                                                                                                                                                                                                                                                                Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.7%;
ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          subunit
                                                                                                                                                                                                                                                                                                         Arthropoda; Tracheata; Hexapoda; Inseq; Endopterygota; Coleoptera; Adephaga;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oxidoreductase; Ubiquinone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40914 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        xrthropoda; Tracheata; Hexapoda; Insecta;
Endopterygota; Coleoptera; Adephaga; Carabidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15,
20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=THORAX MUSCLE;
Su Z.H., Osawa S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 7;
Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
  UBIQUINONE -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8D548DA4BAF52A11 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UBIQUINONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Islands inferred from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      update)
NAD(+) + UBIQUINOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAD(+) + UBIQUINOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                    Insecta;
                                                     Osawa S.;
om a phylogenetic
Carabidae).";
                                                                                                                                                                                                                                                                                                               Carabidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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RESULT
QMDR3
ID Q9
AC Q9
AC Q9
AC Q9
CO Q1
DT 01
DT 01
CO Q1
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Q9MDR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Formation of the Japanese Carabina Fauna inferred from a phylogenetic tree of mitochondrial ND5 gene sequences (Coleoptera, Carabidae).";
J. MO1. EVO1. 50:541-549(2000).
-i- CATALYTIC ACTIVITY: NACH + UBIQUINONE = NAD(+) + UBIQUINOL.
EMBL; AB041084; BAA94643.1;
-. EMBL; AB041083; BAA94642.1;
-. InterPro; IPR001750; Oxidored_q1.
Pfam; PF00361; oxidored_q1.
                                                                                                                                                                                                                                        Q9MDR3;
                                                                                                                                                  01-OCT-2000 (TrEMBLrel. 15, C
01-OCT-2000 (TrEMBLrel. 15, I
01-MAR-2002 (TrEMBLrel. 20, I
NADH dehydrogenase subunit 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence up
01-MAR-2002 (TrEMBLrel. 20, Last annotation
NADH dehydrogenase subunit 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AB041067; BAA94626.1; -.
EMBL; AB041066; BAA94625.1; -.
InterPro; IPR001759; Oxidored_q1.
Pfam; PF00361; Oxidored_q1; 1.
Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
  Carabus.
NCBI_TaxID=120935;
                                             Pterygota;
                                                                                                            Carabus schrencki.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pterygota;
Carabus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9MDR4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9MDR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                 Eukaryota;
                                                                                        Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mitochondrion; NAD; Oxidoreductase; Ubiquinone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=120937;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carabus munakatai.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PISSUE=THORAX MUSCLE;
                                                                                                                                                                                                                                                                                                                                                                            157
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                                                                                                                                                                                                                                                                                                            43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 FIFILFF 26
                                                                                                                                                                                                                                                                                                                                                                                                                  20 FIFLLFF 26
                                                                                                                                                                                                                                                                                                                                                                         FIFLLEF 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FIFLLFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   355
                                             Neoptera;
                                                                 Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neoptera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         355 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40860 MW;
                                             Arthropoda; Tracheata; Hexapoda; Insecta; 
; Endopterygota; Coleoptera; Adephaga; Carabidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.7%; 5c.
100.0%; Pr
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arthropoda; Tracheata; Hexapoda; Insecta; Endopterygota; Coleoptera; Adephaga; Carabidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40895 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                  Last sequence update)
Last annotation updat
5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 7;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 68 
Mismatches
                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         927E920321AE5665 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   956C1181F08A06FF CRC64;
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8d
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68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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RP SEQUENCE FROM N.A.

RC TISSUE-THORAX MUSCLE;

RC MEDLINE-20296815; PubMed-10835484;

RX MEDLINE-20296815; PubMed-10835484;

RX Tominaga O., Su Z.H., Kim C.G., Okamoto M., Imura Y., Osawa S.;

RT Tominaga O., Su Z.H., Kim C.G., Okamoto M., Imura Y., Osawa S.;

RT Tree of mitochondrial ND5 gene sequences (Coleoptera, Carabidae).";

RT J. Mol. Evol. 50:541-549(2000).

CC I.- CAFALYTIC ACTIVITY: NADH + UBIQUINONE - NAD(+) + UBIQUINOL.

CE MBL; AB041081; BAA94640.1; -.

DR EMBL; AB041081; BAA94639.1; -.

DR InterPro; IRR001750; Oxidored_q1.

RIMITOCHONDRION: NAD; Oxidored_q1.

KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
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Matches 7
                                                    Matches
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01-OCT-2000
01-OCT-2000
01-MAR-2002
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

STRAIN-12, 1, 2, 3, 4, 5, 6, 9, 10, AND 11; TISSUE-THORAX MUSCI
Kim C.G., Tominaga O., Su Z.H., Osawa S.;

"Origin and Diversification of Euleptocarabus porrecticollis
(Coleoptera, Carabidae) in the Japanese Islands inferred from
Mitochondrial ND5 Gene Sequences.";

Mol. Phylogenet. Evol. 0:0-0(1999).

"Mol. Phylogenet. Evol. 0:0-0(1999).

"III CARALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
                                                                                                                                                                                   EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                           InterPro; IPR001750; Oxidore
pfam; PF00361; oxidored_q1;
                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9MDD3
                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carabus porrecticollis porrecticollis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NADH dehydrogenase
                                                                                                                   NON_TER
                                                                                                                                Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pterygota; Neoptera;
                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=87295;
 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      157 FIFLLFF 163
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                        20
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                                                                                                                                                                                L; AB022565; BAA74477.1;
AB022555; BAA74467.1;
AB022556; BAA74468.1;
AB022557; BAA74469.1;
AB022558; BAA74470.1;
AB022559; BAA74471.1;
AB022569; BAA74471.1;
AB022560; BAA74472.1;
AB022560; BAA74474.1;
AB022563; BAA74474.1;
AB022563; BAA74474.1;
AB022563; BAA74474.1;
AB022563; BAA74474.1;
                        FIFLLFF 26
 FIFLLFF 163
                                                                                                                                                          AB022564; BAA74476.1; -.
Pro; IPR001750; Oxidored_
                                                   Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 7; Conserv
                                                                                                    355 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              355 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 20, Last annotation updat
ogenase subunit 5 (Fragment).
                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                              NAD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arthropoda; Tracheata; Hexapoda; Insecta; Endopterygota; Coleoptera; Adephaga; Car
                                             3.7%; >--
100.0%; Pr
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100.0%; Pr
0;
                                                                                                                             Oxidoreductase; Ubiquinone.
                                                                                                      40916 MW;
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                                                                                                                                                         Oxidored_q1.
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                                                              Score 7; 1
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                    E6B39DF6723A8FEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            977A20EC3532FD9C CRC64;
                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                      AND 11; TISSUE-THORAX MUSCLE; wa S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Coleoptera; Adephaga; Carabidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       355
                                                               DB 8;
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Best Local
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
NADH dehydrogenase subunit 5 (Fragment).
                                                                                                                                                                                                                                                                                                      Eukaryota; l
Pterygota;
                                                                                                                                                              STRAIN-HOKKAIDO-KUSHIRO2, AND HOKKAIDO-NEMURO1; TISSUE-THORAX MUSCLE; Su Z.H., Tominaga O., Saito S., Kim C.G., Osawa S.; "Phylogeny of Tomocarabus opaculus (Coleoptera, Carabidae) as deduced
                                                                                                                          InterPro; IPR001750; Oxidored_q1.

Pfam; PF00361; oxidored_q1; 1.

Mitochondrion; NAD; Oxidoreductase; Ubiquinone
NON TER

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F071F1D770E4FED4
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                            Mitochondrion.
                                                                                                                                                                                                                                                                                                                                       Carabus opaculus.
                                                                                                                                                                                                                                                                                                                                                                                                                Q9MDB8
                                                                                                                                                                                                                                                                                   NCBI_TaxID=118064;
                                          157
                                                              20 FIFLLFF 26
                                          FIFLLFF
                                                                                 Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                         Neoptera;
                                                                                                                                                                                                                                                                                                                  Metazoa;
                                                                                   Conservative
                                          163
                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                       Arthropoda; Tracheata; Hexapoda; Insecta; ; Endopterygota; Coleoptera; Adephaga; Carabidae;
                                                                                            3.7%;
       9,
          2002,
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                                                                                            Score 7; [
Pred. No.
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                                                                                   Mismatches
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Carabidae) as deduced
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